

REFERENCE LISTING



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<12> Novel Methods for Therapeutic Vaccination

<13> 3631-0109P

<14> US 59/526, 003

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<151> 1999-10-05

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<150> US 60/105,011

<151> 1998-10-20

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<170> Patent In Ver. 3.0

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 Arg Thr Arg Thr Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Thr
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 Phe Leu Leu Gly Ile Leu His Gly Thr Phe Ile Lys Ser Ser Arg Arg
 45 50 55 60 65

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Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala His Leu Asp Val	
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Leu Lys Ala His Asn Ile Lys Lys His Leu Lys Asn His Thr Val Leu	
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Pro His Leu Ala Gly Thr Gln Gln Asn His Gln Leu Ala Lys His Ile	
aaa att att att att att gga att att att att att att att att att att	152
Gln Ser Gln Trp Lys Gln Phe Gly Leu Asp Ser Val Gln Leu Ala His	
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Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile	
tca ata att aat gaa gat gga aat gat att att aat aat aat att att att	160
Ser Ile Ile Asn Gln Asp Gly Asn Gln Ile Phe Asn Thr Ser Leu Phe	
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Glu Pro Pro Pro Pro Gly Tyr Gln Asn Val Ser Asp Ile Val Pro Pro	
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Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Gln Gly Asp Leu Val Tyr	
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Val Asn Tyr Ala Arg Thr Gln Asp Phe Phe Lys Leu Gln Arg Asp Met	
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Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val	
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Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly	
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Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys	
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Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly	
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Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr	
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Pro Ala Asn Gln Tyr Ala Tyr Arg Arg Gly Ile Ala Gln Ala Val Gly	
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His Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Gln Val	

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Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	
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Stop	Ile	Ala	Stop	Lys	Phe	Ser	Stop	Arg	Leu	Stop	His	Asp	Phe	Asp	Lys	Stop

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 110 Val Ser Lys Lys Ser Asp Trp Ala Arg Lys His Ala Trp Lys Val Lys
 120 Ser Lys Trp Asp Lys Lys Asn Leu Trp Lys Lys Val His Arg Lys
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 330 Ala His Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
 340 Leu Trp Phe Asp Lys Asn Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
 350 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro His His Met Lys Thr
 360 Tyr Ser Val Ser Phe Asp Ser Leu His Ser Ala Val Lys Asn Thr Thr
 370 His Ile Ala Ser Lys Phe Ser His Arg Leu His Asp Phe Asp Lys Ser
 380 Asn Trp Ile Val Leu Arg Met Met Asn Asp His Leu Thr Thr Thr His

Arg Ala Ile Ile Asp Ile Leu Arg Leu Ile Arg Arg Ile Ile Lys Arg
 His Val Ile Lys Ala Ile Ser Ser His Asn Lys Lys Ala Lys Ile Val
 Ile Ile Arg Ile Lys Asp Ala Leu Ile Arg Ile Ile Ser Lys Val Arg
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 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
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 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
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 ttc tac tgg ggc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc 192
 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
 30 35 40 45 50 55 60
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 Leu Pro Thr Asn Ala Ser Leu Ser His Leu Gln Asp Ile Gln Gln Val
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 gag gcc tac tgg ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 288
 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
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 gag agg tgg tgg att tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc 336
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 75 80 85 90 95 100 105
 ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 384
 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Thr
 90 95 100 105 110 115 120
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 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg His Leu Gln Leu Arg Ser
 105 110 115 120 125 130 135 140
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 Leu Thr His Ile Leu Lys Gly Gly Val Leu Ile His Arg Asn Ile Val
 125 130 135 140 145 150 155 160
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 Leu Tyr Lys His Asp Thr Ile Leu Gly Lys Arg Ile Phe His Lys Asn
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5709 5718 5727 5736 5745 5754 5763 5772 5781 5790 5800 5809 5818 5827 5836 5845 5854 5863 5872 5881 5890 5900 5909 5918 5927 5936 5945 5954 5963 5972 5981 5990 6000 6009 6018 6027 6036 6045 6054 6063 6072 6081 6090 6100 6109 6118 6127 6136 6145 6154 6163 6172 6181 6190 6200 6209 6218 6227 6236 6245 6254 6263 6272 6281 6290 6300 6309 6318 6327 6336 6345 6354 6363 6372 6381 6390 6400 6409 6418 6427 6436 6445 6454 6463 6472 6481 6490 6500 6509 6518 6527 6536 6545 6554 6563 6572 6581 6590 6600 6609 6618 6627 6636 6645 6654 6663 6672 6681 6690 6700 6709 6718 6727 6736 6745 6754 6763 6772 6781 6790 6800 6809 6818 6827 6836 6845 6854 6863 6872 6881 6890 6900 6909 6918 6927 6936 6945 6954 6963 6972 6981 6990 7000 7009 7018 7027 7036 7045 7054 7063 7072 7081 7090 7100 7109 7118 7127 7136 7145 7154 7163 7172 7181 7190 7200 7209 7218 7227 7236 7245 7254 7263 7272 7281 7290 7300 7309 7318 7327 7336 7345 7354 7363 7372 7381 7390 7400 7409 7418 7427 7436 7445 7454 7463 7472 7481 7490 7500 7509 7518 7527 7536 7545 7554 7563 7572 7581 7590 7600 7609 7618 7627 7636 7645 7654 7663 7672 7681 7690 7700 7709 7718 7727 7736 7745 7754 7763 7772 7781 7790 7800 7809 7818 7827 7836 7845 7854 7863 7872 7881 7890 7900 7909 7918 7927 7936 7945 7954 7963 7972 7981 7990 8000 8009 8018 8027 8036 8045 8054 8063 8072 8081 8090 8100 8109 8118 8127 8136 8145 8154 8163 8172 8181 8190 8200 8209 8218 8227 8236 8245 8254 8263 8272 8281 8290 8300 8309 8318 8327 8336 8345 8354 8363 8372 8381 8390 8400 8409 8418 8427 8436 8445 8454 8463 8472 8481 8490 8500 8509 8518 8527 8536 8545 8554 8563 8572 8581 8590 8600 8609 8618 8627 8636 8645 8654 8663 8672 8681 8690 8700 8709 8718 8727 8736 8745 8754 8763 8772 8781 8790 8800 8809 8818 8827 8836 8845 8854 8863 8872 8881 8890 8900 8909 8918 8927 8936 8945 8954 8963 8972 8981 8990 9000 9009 9018 9027 9036 9045 9054 9063 9072 9081 9090 9100 9109 9118 9127 9136 9145 9154 9163 9172 9181 9190 9200 9209 9218 9227 9236 9245 9254 9263 9272 9281 9290 9300 9309 9318 9327 9336 9345 9354 9363 9372 9381 9390 9400 9409 9418 9427 9436 9445 9454 9463 9472 9481 9490 9500 9509 9518 9527 9536 9545 9554 9563 9572 9581 9590 9600 9609 9618 9627 9636 9645 9654 9663 9672 9681 9690 9700 9709 9718 9727 9736 9745 9754 9763 9772 9781 9790 9800 9809 9818 9827 9836 9845 9854 9863 9872 9881 9890 9900 9909 9918 9927 9936 9945 9954 9963 9972 9981 9990 10000

100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
Val	Arg	Val	Arg	Gly	Ala	Val	Leu	Gly	Leu	Tyr	Leu	Tyr	Val	Asn	Lys					
1		1						1					11							
121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	
Lys	Gly	Lys	Leu	Ile	Ala	Lys	Ser	Asn	Gly	Lys	Gly	Lys	Asp	Gly	Val					
141		142											143							
144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	
Ile	Thr	Ile	Ile	Val	Leu	Ala	Asn	Asn	Tyr	Thr	Ala	Leu	Gln	Asn	Ala					
164		165									166									
167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	
Lys	Tyr	Ala	Gly	Tyr	Tyr	Met	Ala	Phe	Thr	Arg	Lys	Gly	Arg	Leu	Arg					
187										188										
189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	
Lys	Gly	Leu	Lys	Thr	Arg	Gln	His	Gln	Arg	Gln	Val	His	Gln	Met	Lys					
			196						197											
209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	
Arg	Leu	Pro	Arg	Gly	His	His	Thr	Glu	Gln	Ser	Leu	Arg	Phe	Glu						
			211					212												
229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	
Val	Gln	Asn	Thr	Pro	Pro	Phe	Thr	Arg	Ser	Leu	Arg	Gly	Ser	Gln	Arg					
		235					236													
249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	
Thr	Thr	Ala	Pro	Gln	Pro	Arg														
		251				252														

4119-6
 4119-115
 4119-187
 4119-Homo sapiens

Met	Gly	Ser	Pro	Arg	Ser	Ala	Leu	Ser	Cys	Leu	Leu	Leu	His	Leu	Leu
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Val	Leu	Cys	Leu	Gln	Ala	Gln	Val	Thr	Val	Gln	Ser	Ser	Ser	Pro	Phe
			21					25						3	
Thr	Gln	His	Val	Arg	Gln	Gln	Ser	Leu	Val	Thr	Asp	Gln	Leu	Ser	Arg
		35					40					43			
Arg	Leu	Ile	Arg	Thr	Tyr	Gln	Leu	Tyr	Ser	Arg	Thr	Ser	Gly	Lys	His
		51				55					61				
Val	Gln	Val	Leu	Ala	Asn	Lys	Arg	Ile	Asn	Ala	Met	Ala	Gln	Asp	Gly
		65				72			75					81	
Asp	Pro	Phe	Ala	Lys	Leu	Ile	Val	Gln	Thr	Asp	Thr	Phe	Gly	Ser	Arg
			86					90						93	
Val	Arg	Val	Arg	Gly	Ala	Gln	Thr	Gly	Leu	Tyr	Ile	Cys	Met	Asn	Lys
		100						103				111			
Lys	Gly	Lys	Leu	Ile	Ala	Lys	Ser	Asn	Gly	Lys	Gly	Lys	Asp	Lys	Val
		111					117					121			
His	Thr	Gln	Ile	Val	Leu	Gln	Asn	Asn	Tyr	Thr	Ala	Leu	Gln	Asn	Ala
		121				127					134				
Lys	Tyr	Gln	Gly	Arg	Tyr	Met	Ala	Phe	Thr	Arg	Lys	Gly	Arg	Pro	Arg
		134				141				143					147
Lys	Gly	Leu	Lys	Thr	Arg	Gln	His	Gln	Arg	Gln	Val	His	Gln	Met	Tyr
				147				153							
Arg	Leu	Pro	Arg	Gly	His	His	Thr	Thr	Gln	Gln	Ser	Leu	Arg	Pro	Arg
				153				157							

line 101. Asn Tyr Ile Ile Phe Ile Asn Ser Ile Asn Gly Ser Ile Phe

Tyr Ile Asn Ile Ile Ile Asn

101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116

117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132

133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148

149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164

165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180

181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196

197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212

213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228

229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244

atg tgg aac goa ctg cag gac aga tac tac cgg gag gtc ctg gaa caa 40

Met Trp Asn Ala Leu Gln Asp Arg Asp Ser Ala Glu Val Leu Gly His

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

agg cag agt tgg ctg agt gtt ggg aca ctg gtc ctg ggt tta aac gga 80

Arg Gln Arg Trp Leu Arg Val Gly Thr Leu Val Leu Ala Leu Thr Gly

17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32

aac ttc ctc att gac ttc ctg ttt ggg tgg tta aca aaa cct tcc aat 144

Thr Phe Leu Ile Gly Phe Leu Phe Gly Trp Phe Ile Lys Pro Ser Asn

33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48

gaa ggt aat ggt aat gtt tcc cat tcc ggt atg aag aag gag ttt tta 192

Glu Ala Thr Gly Asn Val Ser His Ser Gly Met Lys Lys Glu Phe Leu

49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64

cat gaa ttg aag ggt gac aac atc aca aca ttc tta ttc aat ttc aca 240

His Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr

65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80

agg aca aca aat ttg gca gga aca aca aat aat ttt gag ctt gca aca 288

Arg Thr Pro His Leu Ala Gly Thr Gln Asn Phe Glu Leu Ala Lys

81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96

caa att cat gac cag tgg aaa gaa ttt ggc ctg gat ttg gtt gag tta 336

Gln Ile His Asp Gln Trp Lys Glu Phe Gly Leu Asp Leu Val Glu Leu

97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112

tcc cat tac gat gtc ttg ctg tcc tat aca aat aaa aat cat tct aac 384

Ser His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn

113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128

tat atc tca ata att aat gaa gat gga aat gag att ttc aaa aca tca 432

Tyr Ile Ser Ile Ile Asn Gln Asp Gly Asn Gln Ile Phe Lys Thr Ser

129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144

tta tct gaa cag aca ctc cca gga tat tag aat ata tca gat ata gag 480

Leu Ser Glu Gln Phe Phe Pro Gly Tyr Gln Asn Ile Ser Asp Val Val

145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160

cca cca tcc agt aac ttc tct cca cca ttc aca cca gag agt aat cta 528

Pro Pro Tyr Ser Ala Phe Ser Pro Gln Gly Thr Pro Ala Gly Asp Leu

161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176

ttg tat gtc aat tat gca cca aat gaa tat ttc ttc aca ctc taa ttc 576

Val Tyr Val Asn Tyr Ala Arg Thr Gln Asp Phe Phe Lys Leu Gln Arg

177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192

taa atg aat gtc aat tat ttc ttc ttg aat ttc ttc ttc ttc aca tat ttc 624

Ala Met Lys Ile Ser Tyr Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly

193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208

aaa ttc ttc aca ttc aat ttc ttc ttc aca aat ttc ttc ttc ttc ttc ttc 672

Ala Phe Phe Ala Phe Asn Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe

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499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	
520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	
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562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	
583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	
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625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	
646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	
667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	
688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	
709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	
730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	
751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	
772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	
793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	
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877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	
898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	
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940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	
961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	
982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000			

Arg	Leu	Val	Val	Val	Gly	Ser	Gly	Asn	Asp	Leu	Val	Val	Val	Phe	Val	
141					142											
Arg	Leu	Val	Val	Val	Ala	Val	Gly	Arg	Ala	Asp	Val	Val	Val	Val	Val	143
144					145											
Thr	Asn	Lys	Val	Val	Val	Tyr	Pro	Leu	Tyr	His	Val	Val	Tyr	Glu	Thr	146
147					148											
Tyr	Glu	Leu	Val	Val	Lys	Phe	Tyr	Asp	Pro	Thr	Thr	Lys	Tyr	His	Leu	149
151					152											
Thr	Val	Ala	Glu	Val	Arg	Gly	Ala	Met	Val	Thr	Glu	Leu	Ala	Asn	Ser	153
154					155											
Ile	Val	Leu	Pro	Phe	Asp	Cys	Gln	Ser	Tyr	Ala	Val	Ala	Leu	Lys	Lys	156
159					160											
Tat	Ggt	Gac	Aat	Ata	Tac	Aat	Att	Tca	Atg	Aaa	Tat	Tca	Caa	Gaa	Atg	161
164					165											
Tyr	Ala	Asp	Thr	Ile	Tyr	Asn	Ile	Ser	Met	Lys	His	Pro	Gln	Glu	Met	166
169					170											
Aag	Gct	Tac	Atg	Ata	Tca	Ttt	Gat	Tca	Ctg	Ttt	Tct	Tca	Gtc	Aat	Aat	171
174					175											
Phe	Thr	Asp	Val	Ala	Ser	Lys	Phe	Asn	Gln	Arg	Leu	Gln	Gln	Leu	Asp	176
179					180											
Aaa	Agc	Aac	Cac	Ata	Tta	Ctg	Aga	Att	Atg	Aat	Gat	Cag	Ctg	Atg	Tat	181
184					185											
Arg	Gaa	Cgt	Gca	Ttr	Att	Gat	Tct	Tta	Ggt	Tta	Tca	Gga	agg	Cct	Ttc	186
189					190											
Tac	agg	Cat	Aac	Att	Tat	Gct	Tca	Agc	Aac	Cat	Aat	Cag	Tat	Gca	Gga	191
194					195											
Gaa	Tca	Ttc	Cct	Ggg	Att	Tat	Gat	Gcc	Ctt	Ttt	Gat	Ata	agt	agc	Aaa	196
199					200											
Gtc	Aat	Gct	Tct	Aag	Cgt	Tgg	Aac	Gaa	Gtg	Aag	Aaa	Cag	Att	Tct	Att	201
204					205											
Gca	Aac	Ttt	Aca	Gtg	Caa	Gct	Gca	Gca	Gag	Aat	Ctg	agg	Gaa	Gta	Gct	206
209					210											

2108-4
 2110-782
 2112-ERT
 2113-Mus musculus

2114-4
 Met Trp Asn Ala Leu Glu Asp Arg Asp Glu Ala Val Val Leu Gly His
 2115-4
 Arg Glu Arg Trp Leu Arg Val Gly Thr Leu Val Leu Ala Leu Thr Gly
 2116-4
 Thr His Leu Ile Gly Thr Leu Phe Gly Thr Thr Thr Lys Trp Val Asn

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Asn	Lys	Thr	His	Leu	Asn	Lys	Leu	Asn	Leu	Leu	Asn	His	Asp	Lys	Asn				
121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140
His	Leu	Leu	Lys	Thr	Asn	Leu	Asn	Leu	Leu	Leu	Leu	Gly	Tyr	Leu					
141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160
Asn	Leu	Asn	Asp	Val	Val	Leu	Pro	Tyr	Asn	Ala	Leu	Asn	Leu	Pro	Gln	Gly			
161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
Thr	Pro	Gln	Gly	Asp	Leu	Val	Tyr	Val	Asn	Lys	Ala	Arg	Thr	Gln	Asp				
181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200
Phe	Phe	Lys	Leu	Gln	Arg	Gln	Met	Lys	Leu	Ser	Cys	Ser	Gly	Lys	Leu				
201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220
Gly	Asn	Gln	Ala	Tyr	Gly	Lys	Val	Phe	Arg	Gly	Asn	Met	Val	Lys	Asn				
221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240
Gly	Asn	Gln	Ala	Tyr	Gly	Lys	Val	Phe	Arg	Gly	Asn	Met	Val	Lys	Asn				
241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260
Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Met	Leu	Leu	Tyr	Ser	Asp	Pro	Ala				
261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280
Gly	Asn	Gln	Ala	Tyr	Gly	Lys	Val	Phe	Arg	Gly	Asn	Met	Val	Lys	Asn				
281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
Asp	Tyr	Phe	Val	Pro	Ala	Val	Lys	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu				
301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320
Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly	Asn	Val	Leu	Asn	Leu	Asn	Gly	Ala				
321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340
Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr	Pro	Ala	Asn	Gln	His	Ala	Tyr	Arg				
341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360
Asn	Gln	Leu	Thr	Asn	Ala	Val	Gly	Leu	Pro	Ser	Leu	Pro	Val	His	Leu				
361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380
Ala	Gln	Tyr	Asp	Asp	Ala	Gln	Lys	Leu	Leu	Gln	His	Met	Gly	Gly	Pro				
381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400
Gly	Pro	Pro	Asp	Ser	Ser	Trp	Lys	Gly	Gly	Leu	Lys	Val	Pro	Tyr	Asn				
401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420
Val	Gly	Pro	Gly	Phe	Ala	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met				
421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440
His	Leu	His	Ser	Tyr	Thr	Lys	Val	Thr	Arg	Leu	Tyr	Asn	Val	Leu	Gly				
441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460
Thr	Leu	Lys	Gly	Ala	Leu	Ala	Pro	Asp	Arg	Tyr	Val	Leu	Gly	Gly					
461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480
His	Arg	Asp	Ala	Trp	Val	Leu	Gly	Gly	Leu	Asp	Pro	Gln	Ser	Gly	Ala				
481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500
Ala	Val	Val	His	Gln	Leu	Val	Arg	Ser	Leu	Gly	Thr	Leu	Lys	Lys	Lys				
501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520
Gly	Arg	Arg	Leu	Arg	Arg	Thr	Leu	Leu	His	Asn	Thr	Lys	Asp	Ala	His				

aaa ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt	11
Glu Asp Gly Ser Ser Gly Ser Thr Ser Asp Ala Ser Ser Glu Ser Asn	
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aaa ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt	12
Leu Ser Ala Ser Asn Gly Val Ala Tyr Leu Asn Asn Asn Ser Ser Leu	
412	
aaa ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt	13
Glu Gly Asn Tyr Thr Leu Arg Val Asn Lys Thr Ser Leu Met Tyr Ser	
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ttt gtt tat aat tta tta aaa gag ctg tta agt tta gtt tta gtt ttt	14
Leu Val Tyr Asn Leu Thr Lys Glu Leu Ser Ser Ser Asn Glu Gly Phe	
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gaa gga aaa ttt ttt tat gag agc tgg aaa gaa gag agt ttt tta ttt	15
Glu Gly Lys Ser Leu Tyr Asp Ser Trp Lys Glu Lys Ser Pro Ser Pro	
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gag ttt att gga atg ttt aga att agt gag ctg ggt ttt ggc aat gat	16
Glu Phe Ile Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp	
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ttt gaa gtt ttt ttt caa aga ttt gga att ggt tta ggt aga ggc gga	17
Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg	
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tat act aaa aat tgg aaa act aac aaa gtc agc agt tat cct ctc tat	18
Tyr Thr Lys Asn Trp Lys Thr Asn Lys Val Ser Ser Tyr Pro Leu Tyr	
418	
cac agt gtc tat gag aca tat gag ctg tta gta aaa ttt tat gac cca	19
His Ser Val Tyr Glu Thr Tyr Glu Leu Val Val Lys Phe Tyr Asp Pro	
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aca ttt aaa tac cac ctc act gtg gcc gag gtt tga gga ggc atg gta	20
Thr Phe Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Ala Met Val	
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ttt gaa ttt gcc aat ttt ata gtg ttt cct ttt tat tgc caa agt tat	21
Phe Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Tyr Gln Ser Tyr	
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ggt gta ggt ctg aag gag tat gct gag act tta tac aat att tca atg	22
Ala Val Ala Leu Lys Tyr Ala Asp Thr Ile Tyr Asn Ile Ser Met	
422	
aaa cat cca caa gaa atg aag gct tac atg ata tta ttt gat tca ctg	23
Lys His Pro Gln Glu Met Lys Ala Tyr Met Ile Ser Phe Asp Ser Leu	
423	
ttt ttt gga gtt aat aat ttt aca gat gtt gga ttt gag ttt aat gag	24
Phe Ser Ala Val Asn Asn Phe Thr Asp Val Ala Ser Lys Phe Asn Gln	
424	
aga ctg caa gag tta cac aaa agc aac ggc ata tta ctg aga att atg	25
Arg Leu Gln Gln Leu Asp Lys Ser Asn Pro Ile Leu Leu Arg Ile Met	
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aat gag gag tta atg tat ctg gaa agt tta ttt aat tat cct tta ggt	26
Asn Asp Gln Leu Met Tyr Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly	
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tta cca gga agt ttt ttt tac agg tat ttt ttt ttt ttt tta ttt agt	27
Leu Pro Gly Arg Ser Phe Tyr Arg His Thr Ile Tyr Ala Pro Ser Ser	
427	
gat aat aat tat tta tta gaa tta ttt ttt ttt ttt ttt ttt ttt	28
His Asn Lys Tyr Ala Gly Gln Ser Phe Pro Gly Leu Tyr Asp Ala Leu	
428	
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Phe Asp Ile Ser Ser Lys Val Asn Ala Ser Tyr Asn Asp Glu Val	
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 Met Tyr Ile Lys Ala Asn Ser Lys Phe Ile Ile Ile Ile
 1 5 10 15

<211> 11
 <212> PRT
 <213> Clostridium tetani

<410> 11
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Ile Ile Thr Glu Leu
 1 5 10 15

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 <213> Clostridium tetani

<210>
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 <222> (1)..(63)

<410> 13
 att aac aac att aac gta agt ttc tgg atg agt gtt cgg aaa gtt agc 43
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
 1 5 10 15
 gat agc cac atg gaa 63
 Ala Ser His Leu Glu
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 <213> Clostridium tetani

<410> 14
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 Ala Ser His Leu Glu
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<210> 17
 <211> 17
 <212> PRT
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<210> Description of Artificial Sequence: Fusion of
 the amino-terminal region of the

<210> 16
 His Val Arg Gly Val Ala Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
 1 5 10 15
 Ile Thr Glu Leu Arg Val Arg Tyr Thr

<210> 16
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion of
 tetanus toxoid epitope and PSM

<400> 16
 Ala Val Val Leu Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
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 Ile Thr Glu Leu Glu Met Lys Thr Tyr
 20 25

<210> 17
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion of
 tetanus toxoid epitope and PSM

<400> 17
 Met Phe Leu Glu Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
 1 5 10 15
 Ile Thr Glu Leu His Val Ile Tyr Ala
 20 25

<210> 16
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion of
 tetanus toxoid epitope and PSM

<400> 16
 Asn Ser Arg Leu Ile Ile Ala Asn Ile Thr Val Ser Phe Thr Ile Arg
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 Val Ile Lys Val Ser Ala Ser His Leu Thr Val Arg Tyr Thr Thr

<210> 14
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of
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<400> 18
Val Val Leu Arg Lys Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
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Val Pro Lys Val Ser Ala Ser His Leu Glu Ser Phe Asn Ser Leu
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<400> 20
Leu Met Phe Leu Glu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
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Val Pro Lys Val Ser Ala Ser His Leu Glu Pro Ser Phe His Asn
20 25 30

<210> 21
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<212> DNA
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<220>
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<221> CDS
<222> (1)..(18)

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His His His His His His
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Year	1990	1991	1992	1993	1994	1995
1990	1991	1992	1993	1994	1995	1996

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423> Description of Artificial Sequence: Artificially
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[illegible]

A.2.1. \mathbb{R}^n
 A.2.2. \mathbb{C}^n
 A.2.3. \mathbb{H}^n
 A.2.4. Arithmetic Sequence

$$Z = \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{1}{2} \sum_{i=1}^n \left(\frac{1}{\sigma_i^2} \left(y_i - \sum_{j=1}^p \beta_j x_{ij} \right)^2 \right) \right)$$
[illegible]

the 1990s, the number of people in the world who are illiterate has increased from 1.2 billion to 1.5 billion. The number of illiterate people in the world is expected to reach 1.7 billion by the year 2015. The number of illiterate people in the world is expected to reach 1.7 billion by the year 2015. The number of illiterate people in the world is expected to reach 1.7 billion by the year 2015.

the 1990s, the number of people in the world who are illiterate has increased from 1.2 billion to 1.5 billion. The number of illiterate people in the world is projected to reach 1.7 billion by the year 2015. The number of illiterate people in the world is projected to reach 1.7 billion by the year 2015. The number of illiterate people in the world is projected to reach 1.7 billion by the year 2015.

100

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Pro Asp Thr Arg

<217> 34
<218> 344
<219> FRT
<220> Artificial Sequence

<221>
<222> Fig. 1B - Various FGF- isoforms

<400> 34
Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
1 5 10
Val Leu Cys Leu Gln Ala Gln Glu Gly Pro Gly Arg Gly Pro Ala Leu
20 25 30
Gly Arg Glu Leu Ala Ser Leu Phe Arg Ala Gly Arg Glu Pro Gln Gly
35 40 45
Val Ser Gln Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His
50 55 60
Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile
65 70 75 80
Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val
85 90 95
Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe
100 105 110
Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val
115 120 125
Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys
130 135 140
Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val Phe Thr Glu
145 150 155 160
Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu
165 170 175
Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser
180 185 190
Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro
195 200 205
Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn
210 215 220
Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp Ala
225 230 235 240
Pro Glu Pro Arg

<210> 35
<211> 215
<212> FRT
<213> Homo sapiens

<223>
<224> Dist. feature
<225> 1..215
<226> Fig. 1 - Wild Type WT FGF-1

14 14 14
 Thr Arg Ser Glu Ser Arg Ser Val His His Met Lys Arg Ser Ser Arg
 14 14 14
 Gly His Ser Thr Thr Glu Ser Ser Ser Arg Phe His His Ser Ser Lys
 14 14 14
 Pro Ser Ser Thr Arg Ser Ser Ser Arg Ser Ser Ser Arg Ser Ser Arg
 14 14 14
 Glu Ser Arg
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<210> 1
 <211> 1
 <212> 1P1
 <213> Artificial Sequence

<220>
 <223> Fig. 6 - FZ1: Internal variant of FGF2b constructed by replacing
 external
 loops in the FGF2 structure with P2 epitope

<400> 37
 Met Ala Glu Val Thr Val Glu Ser Ser Pro Asn Phe Thr Glu His Val
 1 5 10 15
 Arg Glu Glu Ser Leu Val Thr Asp Glu Leu Ser Arg Arg Leu Ile Arg
 20 25 30
 Thr Tyr Glu Leu Tyr Ser Arg Thr Ser Gly Lys His Val Glu Val Leu
 35 40 45
 Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala
 50 55 60
 Lys Leu Ile Val Glu Thr Asp Glu Tyr Ile Lys Ala Asn Ser Lys Phe
 65 70 75 80
 Ile Gly Ile Thr Glu Leu Gly Ser Arg Val Arg Val Arg Gly Ala Glu
 85 90 95
 Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu Ile Ala Lys
 100 105 110
 Ser Asn Gly Lys Gly Lys Asp Cys Val Phe Thr Glu Ile Gly Leu Glu
 115 120 125
 Asn Asn Tyr Thr Ala Leu Glu Asn Ala Lys Tyr Glu Gly Trp Tyr Met
 130 135 140
 Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser Lys Thr Arg Glu
 145 150 155 160
 His Glu Arg Glu Val His Phe Met Lys Arg Leu Pro Arg Gly His His
 165 170 175
 Thr Thr Glu Glu Ser Leu Arg Phe Glu Phe Leu Asn Tyr Pro Thr Phe
 180 185 190
 Thr Arg Ser Leu Arg Gly Ser Glu Arg Thr Trp Ala Pro Glu Pro Arg
 195 200 205

<210> 1
 <211> 1
 <212> 1P1
 <213> Artificial Sequence

<220>
 <223> Fig. 6 - FZ1: Internal variant of FGF2b constructed by replacing

Extending 100% in the F3H8b structure with 100% sequence

```

Met Ala Gln Val Thr Val Gln Ser Ser Pro Asp Phe Thr Gln His Val
1      5      10      15
Arg Gln Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg
20     25     30     35
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
40     45
Ala Asn Lys Arg Ile Asn Ala Met Ala Gln Asp Gly Asp Pro Phe Ala
50     55     60
Lys Leu Ile Val Gln Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65     70     75     80
Gly Ala Gln Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
85     90
Ile Ala Lys Ser Asn Gly Phe Asn Asn Phe Thr Val Ser Phe Trp Leu
95    100    105    110
Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Asp Cys Val Phe Thr
115    120    125
Glu Ile Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr
130    135    140
Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly
145    150    155    160
Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu
165    170    175
Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu
180    185    190
Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp
195    200    205
Ala Pro Gln Pro Arg
210

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<210> 39

<211> 199

<212> PRT

<213> Artificial Sequence

<214>

<215> Fig. 6 -F20: Variant of F3F8b with 10 epitope in the C-terminal

<400> 39

```

Met Ala Gln Val Thr Val Gln Ser Ser Pro Asp Phe Thr Gln His Val
1      5      10      15
Arg Gln Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg
20     25     30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
35     40     45
Ala Asn Lys Arg Ile Asn Ala Met Ala Gln Asp Gly Asp Pro Phe Ala
50     55     60
Lys Leu Ile Val Gln Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65     70     75     80
Gly Ala Gln Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
85     90
Ile Ala Lys Ser Asn Gly Lys Gly Lys Asn Tyr Val Ile Thr Gln Ile
95    100    105    110

```

Gly Leu Ala Asn Asn Tyr Thr Ala Leu Ala Asn Ala Tyr Tyr Ala Gly
 11
 Asp Tyr Thr Ala Ile Thr Arg Tyr Tyr Asn Ile Asn Tyr Tyr Thr Tyr
 12
 Ala Arg Ala His Thr Arg Ala Val His Ile Met Tyr Asn Leu Ile Arg
 13
 Gly His His Thr Thr Ala Gln Ser Leu Asn Ile Ala Ile Leu Asn Tyr
 14
 Pro Pro His Thr Ala Tyr Ile Lys Ala Asn Ser Lys Ile Ile Gly Ile
 15
 Thr Ala Leu Pro Ala Pro Arg
 16

<210> 47
 <211> 13
 <212> PPT
 <213> Artificial Sequence

<220>
 <223> A preferred pan DR epitope (FAFRK) peptide has this sequence
 <400> 41

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
 1 5 1

<210> 41
 <211> 11
 <212> PPT
 <213> Artificial Sequence

<220>
 <223> FAFRb specific peptide
 <400> 41

Gln Val Thr Val Ala Ser Ser Pro Asn Ile Thr
 1 5 1